



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/800,140
Source: FWO
Date Processed by STIC: 3/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/800,140

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 03/23/2004

PATENT APPLICATION: US/10/800,140

TIME: 13:20:09

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03232004\J800140.raw

3 <110> APPLICANT: SYRRX, INC.
 5 <120> TITLE OF INVENTION: PROBE, ASSAY AND KITS FOR DETECTING 11a-HYDROXYSTEROID
 6 DEHYDROGENASE AND MODULATORS THEREOF
 8 <130> FILE REFERENCE: SYR-HSD-5002
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/800,140
 11 <141> CURRENT FILING DATE: 2004-03-11
 13 <160> NUMBER OF SEQ ID NOS: 7
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 292
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 W--> 24 <221> NAME/KEY: Amino acid sequence for full-length human wild type
 W--> 25 11 -hydroxysteroid dehydrogenase
 26 <222> LOCATION: (1)..(292)
 28 <400> SEQUENCE: 1
 30 Met Ala Phe Met Lys Lys Tyr Leu Leu Pro Ile Leu Gly Leu Phe Met
 31 1 5 10 15
 34 Ala Tyr Tyr Tyr Tyr Ser Ala Asn Glu Phe Arg Pro Glu Met Leu
 35 20 25 30
 38 Gln Gly Lys Lys Val Ile Val Thr Gly Ala Ser Lys Gly Ile Gly Arg
 39 35 40 45
 42 Glu Met Ala Tyr His Leu Ala Lys Met Gly Ala His Val Val Val Thr
 43 50 55 60
 46 Ala Arg Ser Lys Glu Thr Leu Gln Lys Val Val Ser His Cys Leu Glu
 47 65 70 75 80
 50 Leu Gly Ala Ala Ser Ala His Tyr Ile Ala Gly Thr Met Glu Asp Met
 51 85 90 95
 54 Thr Phe Ala Glu Gln Phe Val Ala Gln Ala Gly Lys Leu Met Gly Gly
 55 100 105 110
 58 Leu Asp Met Leu Ile Leu Asn His Ile Thr Asn Thr Ser Leu Asn Leu
 59 115 120 125
 62 Phe His Asp Asp Ile His His Val Arg Lys Ser Met Glu Val Asn Phe
 63 130 135 140
 66 Leu Ser Tyr Val Val Leu Thr Val Ala Ala Leu Pro Met Leu Lys Gln
 67 145 150 155 160
 70 Ser Asn Gly Ser Ile Val Val Val Ser Ser Leu Ala Gly Lys Val Ala
 71 165 170 175
 74 Tyr Pro Met Val Ala Ala Tyr Ser Ala Ser Lys Phe Ala Leu Asp Gly
 75 180 185 190
 78 Phe Phe Ser Ser Ile Arg Lys Glu Tyr Ser Val Ser Arg Val Asn Val
 79 195 200 205

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This does
 not belong
 on <221> line.
 Move it to
 <223> line.
 (See 1.823
 of Sequence Rules)

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Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03232004\J800140.raw

82 Ser Ile Thr Leu Cys Val Leu Gly Leu Ile Asp Thr Glu Thr Ala Met
 83 210 215 220
 86 Lys Ala Val Ser Gly Ile Val His Met Gln Ala Ala Pro Lys Glu Glu
 87 225 230 235 240
 90 Cys Ala Leu Glu Ile Ile Lys Gly Gly Ala Leu Arg Gln Glu Glu Val
 91 245 250 255
 94 Tyr Tyr Asp Ser Ser Leu Trp Thr Thr Leu Leu Ile Arg Asn Pro Cys
 95 260 265 270
 98 Arg Lys Ile Leu Glu Phe Leu Tyr Ser Thr Ser Tyr Asn Met Asp Arg
 99 275 280 285
 102 Phe Ile Asn Lys
 103 290

106 <210> SEQ ID NO: 2

107 <211> LENGTH: 286

108 <212> TYPE: PRT

109 <213> ORGANISM: Custom

112 <220> FEATURE:

invalid <2137> response. see item 10 on End Summary Sheet.

W--> 113 <221> NAME/KEY: Amino acid sequence for residues 24-292 of 11 -hydroxysteroid

W--> 114 dehydrogenase with a N-terminal MKHQHQHQHQHQHQOPL tag

115 <222> LOCATION: (1)..(286)

117 <400> SEQUENCE: 2

*move to <2237>
line*

119 Met Lys His Gln His Gln His Gln His Gln His Gln Gln Pro
 120 1 5 10 15
 123 Leu Asn Glu Glu Phe Arg Pro Glu Met Leu Gln Gly Lys Lys Val Ile
 124 20 25 30
 127 Val Thr Gly Ala Ser Lys Gly Ile Gly Arg Glu Met Ala Tyr His Leu
 128 35 40 45
 131 Ala Lys Met Gly Ala His Val Val Val Thr Ala Arg Ser Lys Glu Thr
 132 50 55 60
 135 Leu Gln Lys Val Val Ser His Cys Leu Glu Leu Gly Ala Ala Ser Ala
 136 65 70 75 80
 139 His Tyr Ile Ala Gly Thr Met Glu Asp Met Thr Phe Ala Glu Gln Phe
 140 85 90 95
 143 Val Ala Gln Ala Gly Lys Leu Met Gly Gly Leu Asp Met Leu Ile Leu
 144 100 105 110
 147 Asn His Ile Thr Asn Thr Ser Leu Asn Leu Phe His Asp Asp Ile His
 148 115 120 125
 151 His Val Arg Lys Ser Met Glu Val Asn Phe Leu Ser Tyr Val Val Leu
 152 130 135 140
 155 Thr Val Ala Ala Leu Pro Met Leu Lys Gln Ser Asn Gly Ser Ile Val
 156 145 150 155 160
 159 Val Val Ser Ser Leu Ala Gly Lys Val Ala Tyr Pro Met Val Ala Ala
 160 165 170 175
 163 Tyr Ser Ala Ser Lys Phe Ala Leu Asp Gly Phe Phe Ser Ser Ile Arg
 164 180 185 190
 167 Lys Glu Tyr Ser Val Ser Arg Val Asn Val Ser Ile Thr Leu Cys Val
 168 195 200 205
 171 Leu Gly Leu Ile Asp Thr Glu Thr Ala Met Lys Ala Val Ser Gly Ile
 172 210 215 220

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/800,140

DATE: 03/23/2004

TIME: 13:20:09

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03232004\J800140.raw

175 Val His Met Gln Ala Ala Pro Lys Glu Glu Cys Ala Leu Glu Ile Ile
 176 225 230 235 240
 179 Lys Gly Gly Ala Leu Arg Gln Glu Glu Val Tyr Tyr Asp Ser Ser Leu
 180 245 250 255
 183 Trp Thr Thr Leu Leu Ile Arg Asn Pro Cys Arg Lys Ile Leu Glu Phe
 184 260 265 270
 187 Leu Tyr Ser Thr Ser Tyr Asn Met Asp Arg Phe Ile Asn Lys
 188 275 280 285

191 <210> SEQ ID NO: 3

192 <211> LENGTH: 1405

193 <212> TYPE: DNA

194 <213> ORGANISM: Custom *invalid*

197 <220> FEATURE:

W--> 198 <221> NAME/KEY: Human cDNA sequence encoding residues 24-292 of

W--> 199 11 -hydroxysteroid dehydrogenase *<223> line*

200 <222> LOCATION: (1)..(1405)

202 <400> SEQUENCE: 3

203 acaattcaga ggctgctgcc tgetttaggag gttgtagaaa gctctgtagg ttctctctgt 60
 205 gtgtcctaca ggagtcttca ggccagctcc ctgtcggatg gcttttatga aaaaatatct 120
 207 cctccccatt ctggggctct tcatggccta ctactactat tctgcaaacg aggaattcag 180
 209 accagagatg ctccaaggaa agaaagtgat tgtcacaggg gccagcaaag ggatcggaag 240
 211 agagatggct tatcatctgg cgaagatggg agcccatgtg gtggtgacag cgaggtcaaa 300
 213 agaaactcta cagaaggtgg tatccactg cctggagctt ggagcagcct cagcacacta 360
 215 cattgctggc accatggaag acatgacctt cgcagagcaa tttgttgccc aagcaggaaa 420
 217 gctcatggga ggactagaca tgctcattct caaccacatc accaactctt ctttgaatct 480
 219 ttttcatgat gatattcacc atgtgcgcaa aagcatggaa gtcaacttcc tcagttacgt 540
 221 ggtcctgact gtagctgect tgcccattgt gaagcagagc aatggaagca ttgttgtcgt 600
 223 ctctctctct gctgggaaag tggcttatcc aatggttgct gcctattctg caagcaagtt 660
 225 tgctttggat gggttcttct cctccactag aaaggaatat tcagtgtcca gggccaatgt 720
 227 atcaatcact ctctgtgttc ttggcctcat agacacagaa acagccatga aggcagtttc 780
 229 tgggatagtc catatgcaag cagctccaaa ggaggaaatgt gccctggaga tcatcaaagg 840
 231 gggagctctg cgccaagaag aagtgtatta tgacagctca ctctggacca ctcttctgat 900
 233 cagaaatcca tgcaggaaga tcttgaatt tctctactca acgagctata atatggacag 960
 235 attcataaac aagtaggaac lccctgaggg ctgggcattg tgagggattt tgggactgtt 1020
 237 ctgtctcatg tttatctgag ctcttatcta tgaagacatc ttcccagagt gtcccagag 1080
 239 acatgcaagt catgggtcac acctgacaaa tgggaaggagt tctcttaaca ttgcaaaaat 1140
 241 ggaaatgtaa taataatgaa tgtcatgcac cgctgcagcc agcagttgta aaattgttag 1200
 243 taaacatagg tataattacc agatagttat attaaattta tatcttata atataatat 1260
 245 gtgatgatta atacaatatt aattataata aaggtcacat aaactttata aattcataac 1320
 247 tggtagctat aacttgagct tattcaggat ggtttcttta aaaccataaa ctgtacaaat 1380
 249 gaaatttttc aatatttggt tctta 1405

252 <210> SEQ ID NO: 4

253 <211> LENGTH: 24

254 <212> TYPE: DNA

255 <213> ORGANISM: Custom

258 <220> FEATURE:

W--> 259 <221> NAME/KEY: DNA sequence encoding PCR primer hsd1_24-F *<223> line*

260 <222> LOCATION: (1)..(24)

262 <400> SEQUENCE: 4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/800,140

DATE: 03/23/2004

TIME: 13:20:09

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03232004\J800140.raw

263 aacgaggaat tcagaccaga gatg 24
266 <210> SEQ ID NO: 5
267 <211> LENGTH: 24
268 <212> TYPE: DNA
269 <213> ORGANISM: Custom
272 <220> FEATURE:
W--> 273 <221> NAME/KEY: DNA sequence encoding PCR primer hsd1_292-r <2237 line
274 <222> LOCATION: (1)..(24)
276 <400> SEQUENCE: 5
277 ttacttggtt atgaatctgt ccat 24
280 <210> SEQ ID NO: 6
281 <211> LENGTH: 23
282 <212> TYPE: DNA
283 <213> ORGANISM: Custom
286 <220> FEATURE:
W--> 287 <221> NAME/KEY: DNA sequence encoding PCR primer hsdC272Sqcf <2237 line
288 <222> LOCATION: (1)..(23)
290 <400> SEQUENCE: 6
291 tcagaaatcc atccaggaag atc 23
294 <210> SEQ ID NO: 7
295 <211> LENGTH: 23
296 <212> TYPE: DNA
297 <213> ORGANISM: Custom
300 <220> FEATURE:
W--> 301 <221> NAME/KEY: DNA sequence encoding PCR primer hsdC272Sqcr <2237 line
302 <222> LOCATION: (1)..(23)
304 <400> SEQUENCE: 7
305 gatcttctg gatggatttc tga 23

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/800,140

DATE: 03/23/2004

TIME: 13:20:10

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03232004\J800140.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:24 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:25 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:1
L:113 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:114 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:2
L:198 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:199 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:3
L:259 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:273 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:287 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:301 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7